

3/8



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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/075,460

DATE: 03/01/2002
 TIME: 11:45:56

2.

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3 <110> APPLICANT: MOCKEL, BETTINA
 4 BATHE, BRIGITTE
 5 HANS, STEFAN
 6 KREUTZER, CAROLINE
 7 HERMANN, THOMAS
 8 PFEFFERLE, WALTER
 9 BINDER, MICHAEL
 11 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpsL GENE
 13 <130> FILE REFERENCE: 218472US0X
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/075,460
 C--> 15 <141> CURRENT FILING DATE: 2002-02-15
 15 <150> PRIOR APPLICATION NUMBER: DE 10107230.9
 16 <151> PRIOR FILING DATE: 2001-02-16
 18 <150> PRIOR APPLICATION NUMBER: DE 10162386.0
 19 <151> PRIOR FILING DATE: 2001-12-19
 21 <160> NUMBER OF SEQ ID NOS: 14
 23 <170> SOFTWARE: PatentIn version 3.1
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 26 <211> LENGTH: 1775
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Corynebacterium glutamicum
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (500)..(880)
 33 <223> OTHER INFORMATION:
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 41 tcggttaagg tcagtggcga gcttctttgc tggttcgttt ccttgaggaa cagtcattggg 180
 43 aaccattcta acaagggatt tgggtgtttc tgcggctagc tgataatgtg aacggctgag 240
 45 tcccactctt gtagttggga attgacggca cctcgcactc aagcgcggtg tcgcccctgg 300
 47 ttttccggga cgcgggtggc catgtttgca tttgatgagg ttgtccgtga catgtttggt 360
 49 cgggccccaa aaagagcccc cttttttgcg tgtctggaca ctttttcaaa tccttcgcca 420
 51 tcgacaagct cagccttcgt gtctgtcccc cgggcgtcac gtcagcagtt aaagaacaac 480
 53 tccgaaataa ggatggttc atg cca act att cag cag ctg gtc cgt aag ggc 532
 54 Met Pro Thr Ile Gln Gln Leu Val Arg Lys Gly
 55 1 5 10
 57 cgc cac gat aag tcc gcc aag gtg gct acc gcg gca ctg aag ggt tcc 580
 58 Arg His Asp Lys Ser Ala Lys Val Ala Thr Ala Ala Leu Lys Gly Ser
 59 15 20 25
 61 cct cag cgt cgt ggc gta tgc acc cgt gtg tac acc acc acc cct aag 628
 62 Pro Gln Arg Arg Gly Val Cys Thr Arg Val Tyr Thr Thr Thr Pro Lys
 63 30 35 40

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65 aag cct aac tct gct ctt cgt aag gtc gct cgt gtg cgc ctt acc tcc 676
66 Lys Pro Asn Ser Ala Leu Arg Lys Val Ala Arg Val Arg Leu Thr Ser
67 45 50 55
69 ggc atc gag gtt tcc gct tac atc cct ggt gag ggc cac aac ctg cag 724
70 Gly Ile Glu Val Ser Ala Tyr Ile Pro Gly Glu Gly His Asn Leu Gln
71 60 65 70 75
73 gag cac tcc atg gtg ctc gtt cgc ggt ggt cgt gtt aag gac ctc cca 772
74 Glu His Ser Met Val Leu Val Arg Gly Gly Arg Val Lys Asp Leu Pro
75 80 85 90
77 ggt gtc cgt tac aag atc gtc cgt ggc gca ctg gat acc cag ggt gtt 820
78 Gly Val Arg Tyr Lys Ile Val Arg Gly Ala Leu Asp Thr Gln Gly Val
79 95 100 105
81 aag gac cgc aag cag gct cgt tcc ccg cta cgg cgc gaa gag ggg ata 868
82 Lys Asp Arg Lys Gln Ala Arg Ser Pro Leu Arg Arg Glu Glu Gly Ile
83 110 115 120
85 att aaa aat gcg taaatcagca gctcctaagc gtccagtagt tcaggaccct 920
86 Ile Lys Asn Ala
87 125
89 gtatacaagt ccgagctcgt taccagctc gtaaacaaga tcctcatcgg tggcaagaag 980
91 tccaccgcag agcgcatcgt ctacggtgca ctcgagatct gccgtgagaa gaccggcacc 1040
93 gatccagtag gaaccctcga gaaggctctc ggcaacgtgc gtccagacct cgaagtctgt 1100
95 tccgcgctg ttggtggcgc tacctaccag gtgccagtgg atgttcgccc agagcgcgca 1160
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122 <212> TYPE: PRT
123 <213> ORGANISM: Corynebacterium glutamicum
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131 Ala Lys Val Ala Thr Ala Ala Leu Lys Gly Ser Pro Gln Arg Arg Gly
132 20 25 30
135 Val Cys Thr Arg Val Tyr Thr Thr Thr Pro Lys Lys Pro Asn Ser Ala
136 35 40 45
139 Leu Arg Lys Val Ala Arg Val Arg Leu Thr Ser Gly Ile Glu Val Ser
140 50 55 60
143 Ala Tyr Ile Pro Gly Glu Gly His Asn Leu Gln Glu His Ser Met Val
144 65 70 75 80
147 Leu Val Arg Gly Gly Arg Val Lys Asp Leu Pro Gly Val Arg Tyr Lys

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151 Ile Val Arg Gly Ala Leu Asp Thr Gln Gly Val Lys Asp Arg Lys Gln
152                               100                               105                               110
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161 <212> TYPE: DNA
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164 <220> FEATURE:
165 <221> NAME/KEY: CDS
166 <222> LOCATION: (500)..(880)
167 <223> OTHER INFORMATION:
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173 ttctctcaaa gtgagttgac ctcggaagaa agctgcagaa agttcatcca cgacttggtt 120
175 tcgggttaagg tcagtggcga gcttctttgc tggttcgttt ccttgaggaa cagtcattggg 180
177 aaccattcta acaagggatt tgggtgtttc tgcggctagc tgataatgtg aacggctgag 240
179 tcccactctt gtagttggga attgacggca cctcgactc aagcgcggtg tcgcccctgg 300
181 ttttccggga cgcggtggcg catgtttgca tttgatgagg ttgtccgtga catgtttggt 360
183 cgggccccaa aaagagcccc cttttttgcg tgtctggaca ctttttcaaa tccttcgcca 420
185 tcgacaagct cagccttcgt gttcgtcccc cgggcgtcac gtcagcagtt aaagaacaac 480
187 tccgaaataa ggatggttc atg cca act att cag cag ctg gtc cgt aag ggc 532
188                               Met Pro Thr Ile Gln Gln Leu Val Arg Lys Gly
189                               1                               5                               10
191 cgc cac gat aag tcc gcc aag gtg gct acc gcg gca ctg aag ggt tcc 580
192 Arg His Asp Lys Ser Ala Lys Val Ala Thr Ala Ala Leu Lys Gly Ser
193                               15                               20                               25
195 cct cag cgt cgt ggc gta tgc acc cgt gtg tac acc acc acc cct agg 628
196 Pro Gln Arg Arg Gly Val Cys Thr Arg Val Tyr Thr Thr Thr Pro Arg
197                               30                               35                               40
199 aag cct aac tct gct ctt cgt aag gtc gct cgt gtg cgc ctt acc tcc 676
200 Lys Pro Asn Ser Ala Leu Arg Lys Val Ala Arg Val Arg Leu Thr Ser
201                               45                               50                               55
203 ggc atc gag gtt tcc gct tac atc cct ggt gag ggc cac aac ctg cag 724
204 Gly Ile Glu Val Ser Ala Tyr Ile Pro Gly Glu Gly His Asn Leu Gln
205 60                               65                               70                               75
207 gag cac tcc atg gtg ctc gtt cgc ggt ggt cgt gtt aag gac ctc cca 772
208 Glu His Ser Met Val Leu Val Arg Gly Gly Arg Val Lys Asp Leu Pro
209                               80                               85                               90
211 ggt gtc cgt tac aag atc gtc cgt ggc gca ctg gat acc cag ggt gtt 820
212 Gly Val Arg Tyr Lys Ile Val Arg Gly Ala Leu Asp Thr Gln Gly Val
213                               95                               100                               105
215 aag gac cgc aag cag gct cgt tcc ccg cta cgg cgc gaa gag ggg ata 868
216 Lys Asp Arg Lys Gln Ala Arg Ser Pro Leu Arg Arg Glu Glu Gly Ile
217                               110                               115                               120
219 att aaa aat gcg taaatcagca gctcctaagc gtccagtagt tcaggaccct 920
220 Ile Lys Asn Ala
221                               125

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223 gtatacaagt ccgagctcgt taccagctc gtaaacaaga tcctcatcgg tggcaagaag 980
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229 tcccgcctgt ttggtggcgc tacctaccag gtgccagtgg atgttcgccc agagcgcgca 1160
231 aacaccctcg cactgcgttg gttggtaacc ttcaccgcgc agcgtcgtga gaacaccatg 1220
233 atcgagcgtc ttgcaaacga acttctggat gcagccaacg gccttggcgc ttccgtgaag 1280
235 cgtcgcgaag acaccacaa gatggcagag gccaacgcgc ccttcgctca ctaccgctgg 1340
237 tagtactgcc aagacatgaa agcccaatca cctttaagat caacgcctgc cggcgccctt 1400
239 cacatttgaa taagctggca gcctgcgttt ctccaaggcg actgggcttt tagtctcatt 1460
241 aatgcagttc accgctgtaa gatagctaaa tagaaacact gtttcggcag tgtgttacta 1520
243 aaaaatccat gtcacttgcc tcgagcgtgc tgcttgaatc gcaagttagt ggcaaaatgt 1580
245 aacaagagaa ttatccgtag gtgacaaact ttttaatact tgggtatctg tcatggatac 1640
247 cccggttaata aataagttaa ttaccgtaac caacaagttg gggtagcact gtggcacaag 1700
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254 <210> SEQ ID NO: 4
255 <211> LENGTH: 127
256 <212> TYPE: PRT
257 <213> ORGANISM: Corynebacterium glutamicum
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262 1 5 10 15
265 Ala Lys Val Ala Thr Ala Ala Leu Lys Gly Ser Pro Gln Arg Arg Gly
266 20 25 30
269 Val Cys Thr Arg Val Tyr Thr Thr Pro Arg Lys Pro Asn Ser Ala
270 35 40 45
273 Leu Arg Lys Val Ala Arg Val Arg Leu Thr Ser Gly Ile Glu Val Ser
274 50 55 60
277 Ala Tyr Ile Pro Gly Glu Gly His Asn Leu Gln Glu His Ser Met Val
278 65 70 75 80
281 Leu Val Arg Gly Gly Arg Val Lys Asp Leu Pro Gly Val Arg Tyr Lys
282 85 90 95
285 Ile Val Arg Gly Ala Leu Asp Thr Gln Gly Val Lys Asp Arg Lys Gln
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289 Ala Arg Ser Pro Leu Arg Arg Glu Glu Gly Ile Ile Lys Asn Ala
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295 <212> TYPE: DNA
296 <213> ORGANISM: Corynebacterium glutamicum
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299 <221> NAME/KEY: CDS
300 <222> LOCATION: (702)..(4196)
301 <223> OTHER INFORMATION:
304 <400> SEQUENCE: 5
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309 tcgacgcctc cctcgacgat gcagctgtct ctaagctggg tgcacaggcc gaaagcatcc 180
311 ctgatggaga tgtgagcaaa atcgcaaata ccgtaggtat tgtgatcggg gcggtattgg 240

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317 ggtgcctcgt agaaggggtc aagaagattt ctgggaaacg cgcccggtcg gttggttgct 420
319 aatagcacgc ggagcaccag atgaaaaatc tcccctttac ttccgcgcgc gatttggtata 480
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323 atcaagggtg tttaaaaaaa ccgatttgac aagggtcattc agtgctatct ggagtcgttc 600
325 agggggatcg ggttcctcag cagaccaatt gtcacaaaat accagcggtg ttgatctgca 660
327 cttaatggcc ttgaccagcc aggtgcaatt acccgcgtaga g gtg ctg gaa gga ccc 716
328                                     Val Leu Glu Gly Pro
329                                     1 5
331 atc ttg gca gtc tcc cgc cag acc aag tca gtc gtc gat att ccc ggt 764
332 Ile Leu Ala Val Ser Arg Gln Thr Lys Ser Val Val Asp Ile Pro Gly
333 10 15 20
335 gca ccg cag cgt tat tct ttc gcg aag gtg tcc gca ccc att gag gtg 812
336 Ala Pro Gln Arg Tyr Ser Phe Ala Lys Val Ser Ala Pro Ile Glu Val
337 25 30 35
339 ccc ggg cta cta gat ctt caa ctg gat tct tac tcc tgg ctg att ggt 860
340 Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr Ser Trp Leu Ile Gly
341 40 45 50
343 acg cct gag tgg cgt gct cgt cag aag gaa gaa ttc ggc gag gga gcc 908
344 Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu Phe Gly Glu Gly Ala
345 55 60 65
347 cgc gta acc agc ggc ctt gag aac att ctc gag gag ctc tcc cca atc 956
348 Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu Glu Leu Ser Pro Ile
349 70 75 80 85
351 cag gat tac tct gga aac atg tcc ctg agc ctt tcg gag cca cgc ttc 1004
352 Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu Ser Glu Pro Arg Phe
353 90 95 100
355 gaa gac gtc aag aac acc att gac gag gcg aaa gaa aag gac atc aac 1052
356 Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys Glu Lys Asp Ile Asn
357 105 110 115
359 tac gcg gcg cca ctg tat gtg acc gcg gag ttc gtc aac aac acc acc 1100
360 Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe Val Asn Asn Thr Thr
361 120 125 130
363 ggt gaa atc aag tct cag act gtc ttc atc ggc gat ttc cca atg atg 1148
364 Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly Asp Phe Pro Met Met
365 135 140 145
367 acg gac aag gga acg ttc atc atc aac gga acc gaa cgc gtt gtg gtc 1196
368 Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr Glu Arg Val Val Val
369 150 155 160 165
371 agc cag ctc gtc cgc tcc ccg ggc gtg tac ttt gac cag acc atc gat 1244
372 Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe Asp Gln Thr Ile Asp
373 170 175 180
375 aag tca act gag cgt cca ctg cac gcc gtg aag gtt att cct tcc cgt 1292
376 Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys Val Ile Pro Ser Arg
377 185 190 195
379 ggt gct tgg ctt gag ttt gac gtc gat aag cgc gat tcg gtt ggt gtt 1340
380 Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg Asp Ser Val Gly Val
381 200 205 210

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VERIFICATION SUMMARY

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date